CLAIMS

1. A method of identifying the location of a mutation in the genome of a particular organism, said method comprising:

a) isolating DNA from an organism having a mutated phenotype,

b) contacting said DNA with a panel of restriction enzymes to produce several fragments of said DNA,

c) introducing said fragments of DNA into a non-mutated host organism to transform said non-mutated organism into a mutated organism that expresses the mutated phenotype,

d) determining the transformation frequency by counting number of the originally non-mutated host organisms of step (c) that express said mutated phenotype, and

e) correlating said transformation frequency to the known locations of the restriction enzyme sites of step (b), to provide information regarding the location of said mutation in the genome.

2. The method of claim 1 wherein, the organism is selected from the group consisting of bacteria, fungi, yeast, Plasmodia and multicellular organisms.

3. The method of claim 3 wherein the bacteria is selected from the group consisting of bacteria for which the entire genomic DNA has been determined and bacteria for which the genomic DNA has been partially determined.

4. The method of claim 4 wherein the bacteria for which the entire genomic DNA has been determined is selected from the group consisting of: *Agrobacterium tumefaciens, Caulobacter crescentus, Listeria monocytogenes, Borrelia burgdorferi, Brucella melitensis, Campylobacter jejuni, Clostridium perfringens, Corynebacterium glutamicum, Escherichia coil, Enterococcus faecalis, Helicobacter pylori, Mycoplasma pneumoniae, Mycoplasma genetalium, Pasteurella multocida, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Rickettsia prowazekii, Salmonella enterica, Salmonella typhimurium, Staphylococcus aureus, Streptococcus Pneumoniae, Streptococcus pyogenes, Xanthomonas campestris pv. canpestris, Yersinia pestis, Bacillus subtilis, Deinococcus radiodurans, Haemophilus influenzae, Lactococcus lactis, Neisseria meningitidis, Nostoc sp, Streptococcus mutans, Streptomyces coelicolor,* and *Synechocystis sp.*

5. The method of claim 4 wherein the bacteria for which the entire genomic DNA has been partially determined is selected from the group consisting of : *Acetobacter xylinum, Acholeplasma laidlawii, Acinetobacter baumannii, Actinobacillus pleuropneumoniae, Actinomyces vvscosus, Agrobacterium rhizogenes, Amycolatopsis mediterranei, Amycolatopsis orientalis, Anabaena spp, Azospirillum brasilense, Azotobacter vinelandii, Bacillus cereus, Bacillus parapertussis, Bacillus thuringiensis, Bacillus licheniformis, Bacillus sphaericus, Bacillus thuringiensis, Bacteroides fragilis, Bordetella pertussis, Bradyhizobium japonicum, Brevibacterium flavum, Brevibacterium lactofermentum, Brucella abortus, Butyrivibrio fbrisolvens, Citrobacter freundii, Clavibacter michiganensis, Clostridium botulinum, Clostridium cellulolyticum, Clostridium difficile, Cyanobacterium chroococcidiopsis, Cytophaga johnsonae, Dichelobacter nodosus, Enterobacter aerogenes, Enterobacter agglomerans, Enterococcus hirae, Erwinia carotovora, Francisella spp, Fremyella diplosiphon, Giardia lambia, Klebsiella pneumoniae, Lactobacillus acidophilus, Lactobacillus casei, Lactobacillus delbrueckii, Lactobacillus fermentum, Lactobacillus gasseri, Lactobacillus helveticus, Lactobacillus plantarum, Lactobacillus salivarius, Lactobacillus teuteri, Legionella pneumophila, Leptospira biflexa, Leuconostoc spp, Methylobacterium extorquens, Mannheimia haemolytica, Methylophillus spp, Mycobacterium aurum, Mycobacterium bovis, Mycobacterium smegmatis, Myxococcus xanthus, Pasteurelia haemolytica, Pasteurella trehalosi, Pediococcus acidilactici, Propionibacterium jensenii, Proteus spp, Pseudomonas oleovorans, Rhizobium leguminosarum, Rhodococcus equi, Rhodopseudomonas viridis, Rhodospirillum molischianum, Rochalimaea quintana, Rubrivivax gelatinosus, Saccharopolyspora erythraea, Salmonella senftenburg, Seratia spp, Serpula hyodysenteriae, Spirulina platensis, Streptococcus cremoris, Streptococcus parasanguis, Streptococcus salivarus, Streptococcus sanguis, Sulfolubus Shibatae, Synechococcus sp., Toxoplasma gondii, Vibrio anguillarum, Vibrio spp, Yersinia pseudotuberculosis, Yersinia enterocolitica* and, *Zymomonas mobilis.*

6. The method of claim 3, wherein the multicellular organism is mammalian.

7. The method of claim 1 wherein, the panel restriction enzymes is selected from the group consisting of *Aci*I, *Acl*I, *Afl*III, *Alu*I, *Apo*I, *Ase*I, *Bbv*I, *Bfa*I, *Bsa*AI, *Bsa*HI, *Bsa*JI, *Bsr*FI, *Bss*KI, *Bst*UI, *Bst*YI, *Cac*8I, *Dde*I, *Dra*I, *Fnu*HI, *Fok*I, *Hae*III, *Hha*I, *Hinf*I, *Hpa*II, *Hph*I, *Hpy*188I, *Hpy*99I, *Hpy*CH4III, *Hpy*CH4IV,

*Hpy*CH4V, *Mae*III, *Mbo*II, *Mnl*I, *Mse*I, *Msl*I, *Nla*III, *Nla*IV, *Rsa*I, *Sau*3AI, *Sau*96I, *Sfa*NI, *Sfc*I, *Sml*I, *Ssp*I, *Taq*I, *Tfi*I, *Tse*I, *Tsp*45I, *Tsp*509I, and *Tsp*RI.

8. The method of claim 1 wherein said panel of restriction enzymes comprise 10 to 50 of said restriction enzymes.

9. The method of claim 1 wherein said transformation process of step (c) occurs by a process selected from the group comprising transduction and eletroporation.

10. The method of claim 1 wherein, the mutated phenotype is selected from the group consisting of drug resistance, increased production of proteins, increased ability to degrade waste and increased ability to detect analytes.

11. The method of claim 10 wherein the increased production of proteins comprises increased production of therapeutically useful biologicals, increased production of industrial enzymes and increased production of secondary metabolites.

12. The method of claim 11 wherein the increased production of secondary metabolites comprises secondary metabolites with pharmacological activities.

13. The method of claim 10 wherein the drug resistance is resistance to antibacterial agents.

14. The method of claim 1 wherein, the correlation of said transformation frequency to the known locations of said restriction enzyme sites is obtained by a restriction map print out.

15. The method of claim 1 wherein, the correlation of said transformation frequency to the known locations of said restriction enzyme sites is obtained by a computerized program.

16. A method of identifying the precise locus and identity of a mutation in the genome of a particular organism, said method comprising:

a) isolating DNA from an organism having a mutated phenotype,

b) contacting said DNA with a panel of restriction enzymes to produce several fragments of said DNA,

c) introducing said fragments of DNA into a non-mutated host organism to transform said non-mutated organism into a mutated organism that expresses the mutated phenotype,

d) determining the transformation frequency by counting number of the originally non-mutated host organisms of step c that express said mutated phenotype,

e) correlating said transformation frequency to the known locations of the restriction enzyme sites of step b, to provide information regarding the location of said mutation in the genome,

and further comprising,

f) amplifying candidate locations of said mutation in the genome by Polymerase Chain Reaction (PCR) using DNA from the mutant as template,

g) testing the amplified candidate location for the ability to transform non-mutated host cells,

h) sequencing the amplified candidate location that transform with high frequency, and

i) comparing the sequence of the amplification product to the sequence of the parent strain to precisely identify the locus and the identity of the mutation in the genome of a particular organism.

17. The method of claim 15 wherein, the organism is selected from the group consisting of bacteria, fungi, yeast, Plasmodia and multicellular organisms.

18. The method of claim 15 wherein the bacteria is selected from the group consisting of bacteria for which the entire genomic DNA has been determined and bacteria for which the genomic DNA has been partially determined.

19. The method of claim 15, wherein the multicellular organism is a mammalian.

20. The method of claim 15 wherein, the panel restriction enzymes is selected from the group consisting of *Aci*I, *Acl*I, *Afl*III, *Alu*I, *Apo*I, *Ase*I, *Bbv*I, *Bfa*I, *Bsa*AI, *Bsa*HI, *Bsa*JI, *Bsr*FI, *Bss*KI, *Bst*UI, *Bst*YI, *Cac*8I, *Dde*I, *Dra*I, *Fnu*HI, *Fok*I, *Hae*III, *Hha*I, *Hinf*I, *Hpa*II, *Hph*I, *Hpy*188I, *Hpy*99I, *Hpy*CH4III, *Hpy*CH4IV, *Hpy*CH4V, *Mae*III, *Mbo*II, *Mnl*I, *Mse*I, *Msl*I, *Nla*III, *Nla*IV, *Rsa*I, *Sau*3AI, *Sau*96I, *Sfa*NI, *Sfc*I, *Sml*I, *Ssp*I, *Taq*I, *Tfi*I, *Tse*I, *Tsp*45I, *Tsp*509I, and *Tsp*RI.

21. The method of claim 15 wherein, the mutated phenotype is selected from the group consisting of drug resistance, increased production of proteins, increased ability to degrade waste and increased ability to detect analytes.

22. The method of claim 20 wherein the drug resistance is resistance to antibacterial agents.

23. A computerized method of identifying location of chromosomal mutations in the genome of a particular organism using a computer program, said method comprising:

a) inputting enzyme transformation data into a computer, wherein said enzyme transformation data comprises the results of frequency of transformation of non-mutated host organism after introduction of DNA fragments from a mutated organism, wherein said DNA fragments have been digested by known restriction enzymes,

b) inputting known map of restriction enzyme cleavage sites into said computer,

c) inputting a group of variables that affect frequency of transformation into said computer,

d) correlating inputs of steps a) b), and c) to genome coordinate through said computer program, wherein said computer program scans genome sequence to identify locations of restriction enzyme cleavage sites in the genome that best fit the transformation frequency data, and

e) comparing the transformation frequency data with the genome restriction enzyme cleavage map to identify the location of the mutation.

24. The method of claim 22 wherein the variables of step (c) comprise: (a) the distance of the mutation from the end of the DNA segment (b) the length of the DNA segment and, and (c) in some species the presence of uptake signal sequences.